sequence which had the following nucleotide sequence:

hybridization probe

5'-CGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGTGCCG-3' (SEQ ID NO:413).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO534 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal lung tissue (LIB26).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO534 [herein designated as UNQ335 (DNA48333-1321)] (SEQ ID NO:409) and the derived protein sequence for PRO534.

The entire nucleotide sequence of UNQ335 (DNA48333-1321) is shown in Figure 164 (SEQ ID NO:409). Clone UNQ335 (DNA48333-1321) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 87-89 and ending at the stop codon at nucleotide positions 1167-1169 (Figure 164). The predicted polypeptide precursor is 360 amino acids long (Figure 165). The full-length PRO534 protein shown in Figure 165 has an estimated molecular weight of about 39,885 daltons and a pI of about 4.79. Clone UNQ335 (DNA48333-1321) has been deposited with ATCC on March 26, 1998. It is understood that the deposited clone contains the actual sequence, and that the sequences provided herein are representative based on current sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO534 polypeptide suggests that portions of it possess significant sequence identity with the protein disulfide isomerase, thereby indicating that PRO534 may be a novel disulfide isomerase.

Still analyzing the amino acid sequence of PRO534, the signal peptides is at about amino acids 1-25 of SEQ ID NO:410. The transmembrane domain is at about amino acids 321-340 of SEQ ID NO:410. The disulfide isomerase corresponding region is at amino acids 212-302 of SEQ ID NO:410. The thioredoxin domain is at amino acids 211-227 of SEQ ID NO:410. N-glycosylation sites are at: 165-168, 181-184, 187-190, 194-197, 206-209, 278-281, and 293-296 of SEQ ID NO:410. The corresponding nucleotides can routinely be determined from the sequences provided herein. PRO534 has a transmembrane domain rather than an ER retention peptide like other protein disulfide isomerases. Additionally, PRO534 may have an intron at the 5 prime end.

EXAMPLE 66: Isolation of cDNA Clones Encoding Human PRO697

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43052. Based on this consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO697.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCTGGCTCGCTGCTGCTGCTC-3' (SEQ ID NO:416);

reverse PCR primer 5'-CCTCACAGGTGCACTGCAAGCTGTC-3' (SEQ ID NO:417).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA43052 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-CTCTTCCTCTTTGGCCAGCCCGACTTCTCCTACAAGCGCAGAATTGC-3' (SEQ ID NO:418).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO697 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO697 [herein designated as UNQ361 (DNA50920-1325)] (SEQ ID NO:414) and the derived protein sequence for PRO697.

The entire nucleotide sequence of UNQ361 (DNA50920-1325) is shown in Figure 166 (SEQ ID NO:414). Clone UNQ361 (DNA50920-1325) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 44-46 and ending at the stop codon at nucleotide positions 929-931 (Figure 166). The predicted polypeptide precursor is 295 amino acids long (Figure 167). The full-length PRO697 protein shown in Figure 167 has an estimated molecular weight of about 33,518 daltons and a pI of about 7.74. Clone UNQ361 (DNA50920-1325) was deposited with the ATCC on March 26, 1998. It is understood that the deposited clone contains the actual sequence, and that the sequences provided herein are representative based on current sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO697 polypeptide suggests that portions of it possess significant sequence identity with sFRPs, thereby indicating that PRO697 may be a novel sFRP family member.

Still analyzing the amino acid sequence of PRO697, the signal peptides is at about amino acids 1-20 of SEQ ID NO:415. The cystein rich domain, having identity with the frizzled N-terminus, is at about amino acids 6-153 of SEQ ID NO:415. The corresponding nucleotides can routinely be determined from the sequences provided herein.

EXAMPLE 67: Isolation of cDNA Clones Encoding Human PRO717

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA42829. Based on the DNA42829 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO717.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-AGCTTCTCAGCCCTCCTGGAGCAG-3' (SEQ ID NO:421);

reverse PCR primer 5'-CGGGTCAATAAACCTGGACGCTTGG-3' (SEQ ID NO:422).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA42829 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-TATGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTG-3' (SEQ ID NO:423).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO717 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB229).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO717 [herein designated as UNQ385 (DNA50988-1326)] (SEQ ID NO:419) and the derived protein sequence for PRO717.

The entire nucleotide sequence of UNQ385 (DNA50988-1326) is shown in Figure 168 (SEQ ID NO:419). Clone UNQ385 (DNA50988-1326) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 17-19 and ending at the stop codon at nucleotide positions 1697-1699 (Figure 168). The predicted polypeptide precursor is 560 amino acids long (Figure 169). The full-length PRO717 protein shown in Figure 169 has an estimated molecular weight of about 58,427 daltons and a pI of about 6.86. Clone UNQ385 (DNA50988-1326) has been deposited with the ATCC on April 28, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO717 polypeptide suggests that PRO717 may be a novel 12 transmembrane receptor. The reverse complement strand of DNA50988 has a stretch that matches identically with human regulatory myosin light strand.

Still analyzing the amino acid sequence of SEQ ID NO:420, transmembrane domains are at about amino acids 30-50, 61-79, 98-112, 126-146, 169-182, 201-215, 248-268, 280-300, 318-337, 341-357, 375-387, and 420-441 of SEQ ID NO:420. N-glycosylation sites are at about amino acids 40-43 and 43-46 of SEQ ID NO:420. A glycosaminoglycan attachment site is at about amino acids 468-471 of SEQ ID NO:420. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 68: Isolation of cDNA Clones Encoding Human PRO731

A database was used to search expressed sequence tag (EST) databases. The EST database used herein was the proprietary EST DNA database LIFESEQ™, of Incyte Pharmaceuticals, Palo Alto, CA. Incyte clone 2581326 was herein identified and termed DNA42801. Based on the DNA42801 sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO731.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GTAAGCACATGCCTCCAGAGGTGC-3' (SEQ ID NO:426);

reverse PCR primer 5'-GTGACGTGGATGCTTGGGATGTTG-3' (SEQ ID NO:427).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA42801 sequence